

1 GCGGCAGCGG CGGCGGCTGA GGAGGGCCCG GCCTGCGAGA GCCTCAGTGG
 51 GAGCCGGGCTC AGCCCTCGGC CACCATGTGCG GCGCCGTCGG AGGAGGAGGA
 101 GTAGCGCGGG CTGGTGATGG AGGCGCAGCC GGAGTGGGCTG CGCGCCGAGG
 151 TGAAGCGGCT GTCCACAGAG CTGGCCGAGA CCACGCGTGA GAAGATCCAG
 201 GCGGCCGAGT ACGGGCTGGC GGTGCTCGAG GAGAAGCACC AGCTCAAGCT
 251 GCAGTTCGAG GAGCTCGAGG TGGACTATGA GGCTATCCGC AGCGAGATGG
 301 AGCAGCTCAA GGAGGCCCTT GGACAAGCAC ACACAAACCA CAAGAAGGTG
 351 GCTGCTGACG GAGAGAGCCG GGAGGAGAGC CTGATCCAGG AGTCGGCCTC
 401 CAAGGAGCAG TACTACGTGC GGAAGGTGCT AGAGCTGCAG ACGGAGCTGA
 451 AGCAGTTGCG CAATGTCCTC ACCAACACGC AGTCGGAGAA TGAGCGCCTG
 501 GCCTCTGTGG CCCAGGAGCT GAAGGAGATC AACCAGAATG TGGAGATCCA
 551 GCGTGGCCGC CTGCGGGATG ACATCAAGGA GTACAAATTC CGGGAAGATC
 601 GTCTGCTGCA GGACTACTCG GAAGTGGAGG AGGAGAACAT CAGCGCTGACG
 651 AAGCAAGTGT CTGTGCTCAG ACAGAACCAG GTGGAGTTTG AGGGCTCAA
 701 GCATGAGATC AAGCGTCTGG AGGAGGAGAC CGAGTACCTC AACAGCCAGC
 751 TGGAGGATGC CATCCGCCCTC AAGGAGATCT CAGAGCGGCA GCTGGAGGAG
 801 GCGCTGGAGA CCCTGAAGAC GGAGCGCGAA CAGAAGAACA GCCTGCGCAA
 851 GGAGCTGTCA CACTACATGA GCATCAATGA CTCTTCTACC ACCAGCCACC
 901 TGCATGTCTC GCTGGATGGC CTCAAGTTCA GTGACGATGC TGCCGAGCCC
 951 AACAAACGATG CCGAGGCCCT GGTCAATGGC TTTGAGCAGC GCGGCCTGGC
 1001 CAAGCTGCCA CTGGACAACA AGACCTCCAC GCCCAAGAAG GAGGGCCTCG
 1051 CACCGCCCTC CCCCAGCCTC GTCTCCGACC TACTCAGTGA GCTCAACATC
 1101 TCTGAGATCC AGAAGCTGAA GCAGCAGCTG ATGCAGATGG AGCGGGAAAA
 1151 GCGGGGCCCTG CTGGCAACGC TGCAGGACAC ACAGAAGCAG CTGGAGCACA
 1201 GCGGGGGCTC CCTGTCAGAA CAGCAGGAGA AGGTGACCCG CCTCACAGAG
 1251 AATCTGAGTG CCTGCGGCG CCTGCAGGCC AGCAAGGAGC GGCAGACAGC
 1301 CCTGGACAAC GAGAAGGACC GTGACAGCCA TGAGGATGGG GACTACTACG
 1351 AGGTGGACAT CAACGGGCCT GAGATCTTGG CCTGCAAGTA CCATGTGGCT
 1401 GTGGCTGAGG CTGGCGAGCT CCGCGAGCAG CTCGAAGCAC TGCGCAGCAC
 1451 GCACGAGGCT CGTGAGGCCC AGCACGCCGA GGAGAAGGGC CGCTATGAGG
 1501 CTGAGGGCCA GGAATCTACG GAGAAGGTCT CCCTGCTAGA GAAGGCCAGC

FIGURE 1

1551 CGCCAGGACC GCGAGCTGCT GCCCCGGCTG GAGAAGGAGC TAAAGAAGGT
 1601 GAGCGACGTC GCCGGCGAGA CACAGGGCAG CCTGAGTGTG GCCCAGGATG
 1651 AGCTGGTGAC CTTCAGTGAG GAGCTGGCCA ATCTCTACCA CCACGTGTGC
 1701 ATGTGCAACA ATGAGACACC CAACCGTGTC ATGCTGGACT ACTACCGCGA
 1751 GGGCGAGGC GGGGCCGGCC GCACCGTCC CGGGGGCCGC ACCAGCCCCG
 1801 AGGCGCGTGG CCGGCGCTCA CCCATCTCC TACCCAAGGG GCTGCTGGCT
 1851 CCTGAGGCGG GCCGAGCAGA TGGTGGGACG GGGACAGCA GCCCTCGCC
 1901 TGGCTCCTCA CTGCCATCAC CCCTGAGTGA CCCACGCCGG GAGCCCATGA
 1951 ACATCTACAA CCTGATCGCT ATCATCCGTG ACCAGATCAA GCACCTGCAG
 2001 GCAGCCGTGG ACCGCACCAC GGAGCTGTCA CGCCAGCGCA TTGCCTCTCA
 2051 GGAGCTGGGC CCCGCCGTGG ACAAGGACAA GGAAGCGCTT ATGAGGAGA
 2101 TCCTCAAGCT GAAGTCGCTG CTCAGCACCA AGCGGGAGCA GATCACCACG
 2151 CTGCGCACTG TGCTCAAGGC CAACAAGCAG ACGGCCGAGG TGCCCTTGC
 2201 CAACCTGAAG AGCAAGTATG AGAATGAGAA GGCCATGGTT ACCGAGACCA
 2251 TGATGAAGCT GCGCAATGAG CTCAAGGCCC TCAAGGAGGA CGCAGCCACC
 2301 TTCTCCTCGC TGCGTGCTAT GTTTGCCACC AGGTGTGACG AGTACATTAC
 2351 ACAGCTGGAT GAGATGCAGC GGCAGCTGGC GGCTGTGAG GACGAGAAGA
 2401 AGACCGTGAA CTCGCTGCTG CGCATGGCCA TCCAGCAGAA GCTGGCGCTG
 2451 ACCCAGCGGC TGGAGCTGCT CGAGCTGGAC CATGAGCAGA CCCGCGGTGG
 2501 CCGTGCCAAA GCCGCCCCGA AGACCAAGCC AGCCACACCG AGCCTGTAGA
 2551 GTAGCTGCCA GGAGGACTTG GCCACCCGGC CCTGTACAC TGCAGCCCTT
 2601 TCCCTTTCCC TCTCGTGGCC CACAAGGAGG AAGGAAGGGC AACCTAAAAG
 2651 CCCACTTAGA AACTTTTGG ATATGCCACT GCAATTCTTT TCAAAATAGC
 2701 ATTCCCCAGG TTTTAAATGG GAGGAAAAAA AGCTTTAATG TTGAGCATGC
 2751 TGCGAGCTGC TGCGTGAAAA GGCCTCTGTA TGGGCCGAAG ACCCTTCTTC
 2801 CTGCGCTGCC AGGCTCGCCA GGAGCCCACT GGAACGCCCC ACCACGGGGG
 2851 CTCCTTGTTA CACATGTTCT TTTTATATCC GATCAACCTG TGCACTTTTG
 2901 ATATTTTGAT ATTATATTG CTCCTTAAT TCCTCGCGTA GAGACGGTCT
 2951 CAGGTGCCGT GGTCTATGCT CGTGGTCTG TAGCTGTCCG CCTCAGCTCC
 3001 CACCGTGTTT GTCTGGTGTG AGCACGAGGC AGAGCTGTGT GCTCCATAGC
 3051 GTGTAGCTTT AGACTCGGAG ATGAGTGCTT TGACCCAGCG AGGAGCTCAG
 3101 CTAAGTGAT CCACGCTGTG GTTCAGCAGC CTTTAGATCA TACGGCATTG
 3151 TGGTTCATGT TTGAAATTAC AGATTTTAAA TGCCATGTTT ATTAAGAAAT

3201 CCAGGGTATT CAGATTCTGG GGTTTTTCAT ATTGTATTAT TATTATCTCT
3251 AGGAATAGTT CAATGTAACA AGAAGAAAAC TTGACCTTTG CTCTGGTTAA
3301 AACAGTAATA GGCACCTGAA AAAAAAGAT AAATATTGA ATGAGTAGTA
3351 TTACCTACAA ATTCCAGAAT TTTCTGGGTT TTAGGACGTT GTGAGCATG
3401 ACTGATTAAAC AGAATTTTAT ACAACTGTAC CAATAAAAT CCAATTTGGA
3451 ATTGTTTGT TACTCTGGTT GTTGTGCCAA ATTGTGTAC ACTTAGAAAA
3501 TTCTACAGTC GTCGATTTTT AGGGTGTCT CTTCAACAC CTTTTGTTA
3551 GTAATCATMG CCAGTAGTGC CTTTCATCAGT TAAGGGAGGT GTCCCAGCAC
3601 AGATCATTTCT CAAAAGCGAG CAGGGAAGAG CTAGTGGGCA TGCTGAAGGC
3651 CAGCGTGGAC AGCAGGTGAG GCAGGTGCTC CTCACACCCA GACCTGGGCA
3701 TCTTCATTGA GGGAAAGAAA ACAGTCATTG TGCAAAATTC TGTAGTCAG
3751 TGATTCTTTA CTGCAAAAT CAGGGGCTTA GAAAATGAAA GCAACACAAA
3801 AACCTTGAGT GTGCTTTGGG AACCAAAATG ACCTTCTGGG ACAAGCTGAG
3851 CAAGCTGTAT GAACGCCACG TTTGTGAAGA GCTGAGGTA TCAGGAGGGC
3901 CGACGCTGTG TTGSCATGCG CAGTAGGGGA TGAGGGTAG CCATAGTATT
3951 CTTTGCAAAT GTGAAAGCGA GACATTATAT CTTCTCTGC TTGCTGTAAC
4001 TAATCACTGT TAATTTCAGG AAACAGAACT CATTAAAACT CCTTAGCAAA
4051 CCAGGTCTAC ATCCTGTTTT GTTGTCTGAG TGAGGTTAGT GGGAGTGGTC
4101 AAATTGGTAC TCTTGGAGGA AGAAAACTG TCCTTCCTTC TCCAAAAAG
4151 GAAAAATTAT AATAATATAA ATGACAAAAA TAAAGAAAT CTGTTTCTG
4201 GAATAAGCAT TTCTTATTC TAGTTGTAGG GACTCCTATT TTTACCTCC
4251 GTTACAGTGT TGATTCATAA GAAATATTGT TACATTGAG ATAACCTCAT
4301 CTGTATGGGG TATTTATTGT CAATGATGTC TGAGTACTGT ATTTTTCCTG
4351 TGCATTACCT TAGTGTCAGA ATGTTGTCT TATTTTAAA GTCATATGCA
4401 TGTTCCTCTG CCAAGGAACC TTTCACAGA CCCAAACAAA AAAATAATAA
4451 TCAATGCCT TCAATTTCTG AGAAAATGAG GCAGAGCATG GAAAAGGAAT
4501 AGGAAGGAGA AATTAATTGA GATTTCAGG ACACAGACAT ATGATGTGAA
4551 TGCCTACAAA GCCAGTGTGC ATAGGAACAG TGGGCTGGG TAAAGAGTCA
4601 CATTTGGTAGG

00000106000

1 MSAPSEEEY ARLVMEAQPE WLRAEVKRLS HELAETTREK IQAEYGLAV
 51 LEEKHQKLQ FEELEVDYEA IRSEBQIKE AFQQAHNK KVAADGESRE
 101 ESLIQESASK BQYVVKVLE LQTELQLFN VLTINQSENE RLASVAQELK
 151 EINQVETQR GLRADDIKEY KFEARLLQD YSELEENIS LQKQSVLRQ
 201 NQVEFGLKH EIKRLEETE YINQLEDAI RUKETSERQL EEALETYKTE
 251 REQKSLRKE LSHYMSINDS FYTSHLVSL DGLKPSDDAA EPNDAEALV
 301 NGFEHGLAK LPLNKSTIP KKEGLAPPSP SLVSDLLSEL NISEIQKLQ
 351 QLMQMERKA GLATLQDTQ KQLEHTRGSL SBQEKVIRL TENLSALRL
 401 QASKRQIAL INEKORDSHE DGVYEVNDIN GPEILACKYH VAVAEAGELR
 451 BQKALRSTH EAREQAHEE KGRVEAQQA LTERVSLLEK ASRQORELA
 501 RLEKELKVS DVAGETQSSL SVAQELVTF SEELANLYHH VOMNNETFN
 551 RVMLDYREB QGAGRTSPG GRTSPFARGR RSPILLPKIL LAPEAGRADG
 601 GTGSSPSFG SSLPSPLSDP RREPMNTNVL IALIRQIKH LQAVDRITE
 651 LSPQRIASQE LGPAVDIKE ALMEEILKLE SLLSTKREBI TILRIVLKN
 701 KQIAEVALAN LKSKYENKA MVTEIMMKLR NELKALKEDA ATFSSLRAMP
 751 ATRCDEYTTQ LDEMQRQLAA ADEKKTINS LRMATQQKL ALTQRELE
 801 LHQBQIRRGK AKAAFKIKPA TPLS*

FIGURE 2

1 ATGTGGGTGC TGGGCGAGTA CGAGCGACAC TGCGATTCCA TCAACTCGGA
 51 CTTTGGGAGC GAGTCCGGGG GTTCCGGGGA CTGAGTCCGG GGGCCTAGGG
 101 CCAGTCAGGG GCGCGAGGCC GCGCGCGGGG CGCGCGAGCA GGAGGAACTG
 151 CACTACATCC CCATCCGGGT CCTGGGCGGC GGGCCTTCG GGAAGCCAC
 201 GCTGTACCGC CGCACCGAGG ATGACTCACT GGTGTGTGG AAGGAAGTGG
 251 ATTGACCGG GCTGTCTGAG AAGGAAGTTC GTGATGCCIT GATTCAGATT
 301 GTTATTCTGG CACTGCTCCA GATGACAC ATATTGCTT ACTACATCA
 351 CTTCAITGGC AATACCAAGC TCTGTATTGA GCTGGAATAT TGTAAITGGG
 401 GGAACCTGTA TGACAAAATC CTTGTGAGA AGGCAAGTIT GTTITAGGAA
 451 GAGATGGTGG TTGTGTACTT ATTTCAGATT GTTTCAGCAG TGAGCTGCTT
 501 CCATTAAGCT GGAATCCCTT AATGAGATAT AAAGACATTA AATATTTTTC
 551 TGACCAAGGC AAACCTGATA AAACCTGGAG ATTATGCGCT AGCAAAGAA
 601 CTTATTCTG AGTATTCCAT GCGTGAGAG CTTGTGGGAA CCCCATTATA
 651 CATGTCTCCA GAGCTCTGTC AAGGAGTAA GTACAAITTC AAGTCTGATA
 701 TCTGGGCGAT TGGCTGGTTC ATTTTGTGAC TGCTTACCTT AAAGAGGAG
 751 TTTGATGCTA CAAACCCACT TAACTGTGT GTGAAGATCG TCGAAGGAT
 801 TCGGCGCATG GAAGTTGACT CTAGCCAGTA CTCCTTGGAA TTGATCCAAA
 851 TGGTTCATTC GTGCTTGAC CAGGATCTG AGCAGAGACC TACTGCAGAT
 901 GAATCTCTAG ATCGGCTCTT TCTCAGGAA CGCAGGAGAG AGATGGAGGA
 951 AAAGTCACT CTGCTTATG CACCTACAA GAGACCAAG TCAAGCACTG
 1001 TGACTGAAGC ACGCTTGCT GTAGTACAT CAGCAACAG TGAAGTCTAT
 1051 GTTGGGGTGG GTGGAATAAT CACCCCCAG AACTGGAAT TTATCAAGAG
 1101 TGGCTGTAGT GCGCGCAGG TCTGTGAGG GAATACCCAT TTGTCTGTGG
 1151 TCACAGTGGG GAGGAACTG TACACTTGG TGAACATCA AGGAGGCACT
 1201 AAATCCATG GTGAGCTGG CCATGGAGC AAAGCTCTCT ATGACAGGC

FIGURE 3

1251	AAAGCATGTG	GAAAAGTTGC	AAGGCAAGC	TATCCATCAG	GTGTCTATGT
1301	GTGATGATTT	CAC TTGTCGT	GTGACTGATG	AGGGTCAGCT	CTATGCGCTC
1351	GGATCAGATT	ATTATGGCGT	CATGGGGGTG	GACAAAGTTG	CTGGCGCTGA
1401	AGTGCTAGAA	CCCATGCAGC	TGAACTTCTT	CTTCAGCAAT	CCAGTGGAGC
1451	AGGCTCCTCG	TGGAGATTAAT	CATGTGCTGG	TTCTGACAG	AAACAAGGAA
1501	GTCTATTCTT	GGGCTGTGG	CGAATATGGA	CGACTGGGTT	TGGATTCAGA
1551	AGAGGATTAT	TATACAACAC	AAAAGGTGGA	TGTTCCCAAG	GCGTTGATTA
1601	TTGTTCAGT	TCAATGTGGC	TGTGATGGGA	CATTTCGTGT	GACCGAGTCA
1651	GGCAAGGTGC	TGGCTGTGG	ACTCAATGAA	TTCAATAGC	TGGTCTGAA
1701	TCAGTGCAATG	TGGGAATTA	TCAACCATGA	AGCATACCAT	GAGTTCCCT
1751	ACACAAGTGC	CTTTACCTTG	GCCAAACAGT	TGTCTCTTTA	TAAAGTCCGT
1801	ACCATTTGCC	CAGGCAAGAC	TCACACAGCT	GCTAATGATG	AGCGAGGCGG
1851	GCTGCTGACC	TTTGCTGCA	ACAAGTGTGG	GCAGCTGGGC	GTTCGGAACT
1901	ACAGAGAGGG	TCTGGGAATC	AACTGTGTGG	GGGGACCCCT	TGGTGGGAAG
1951	CAAGTGATCA	GGGTCTCCTG	CGGTGATGAG	TTTACCATTG	CTGGCACTGA
2001	TGATTAATCAC	ATTTTTGCTT	GGGGCAATGG	TGTTAATGGC	CGCCTGGCAA
2051	TGACCCCGAC	AGAGAGACCA	CATGCCCTCG	ATATCTGTAC	CTCATGGCCT
2101	CGGCTATTAT	TTGATCTCTT	GCATCATGTC	CGGACCTGT	CTTGGCGTGG
2151	ATGGCATACC	ATTCTCATCG	TTGAGAAAGT	ATTGAATCTT	AAGACCATCC
2201	GTTCCAATAG	CAGTGGCTTA	TCCATTGGAA	CTGTGTTTCA	GAGCTCTAGC
2251	CCGGGAGGAG	GCGCGGGGGG	CGCGGGTGGT	GAGAGAGAGG	ACAGTCAGCA
2301	GGATCTTGAA	ACTCCTGACC	CAGTGGAGG	CTTCCGAGGA	ACAATGGAGG
2351	CAGACCGAGG	AATGGAAGST	TTAATCAGTC	CCACAGAGGC	CATGGGGAAC
2401	AGTAATGGGG	CCAGCAGCTC	CTGTCTGGC	TGGCTTGAA	AGGAGCTGGA
2451	AAATGCAGAA	TTTATCCCAA	TGCGTGACAG	CCCATCTCCT	CTCAGTCCAG
2501	CGTTTTCAGA	ATCTGAGAAA	GATACCCCTC	CCTATGAAGA	GCTTCAGAGG

2551	CTCAAGTGG	CCTCTGAAGC	TOCTTTGGAA	CACAAACCC	AAGTAGAAGC
2601	CTGTGACCT	CGGCTGAATC	CTGCACTAAC	CTGTGCTGGG	AAGGGACAC
2651	CACCTGACTCC	TOCTGGGTGT	GCGTGACGCT	CTCTGCAGGT	GGAGGTTGAG
2701	AGATTGCAGG	GTCTGGTGT	AAAGTGTCCTG	GCTGACACAC	AGAAGCTACA
2751	GCAAGAAAC	CTOCAGATT	TTACCCAACT	CGAGAGTTG	AACAGAAAT
2801	TAGAAGGAGG	GCAGCAGGTG	GGGATGCATT	CCAAAGGCAC	TCAGACAGCA
2851	AAGGAAGAGA	TGGAATGGA	TOCAAGGCT	GACTTAGATT	CAGATTCTTG
2901	GTGGCTCTTG	GGACAGACT	CCTGTAGACC	CAGCCTCTAG	

1 MSLVGEYERH CDSINSDFGS ESGGCGDSSP GPSASQGPRA GGGAAEQEEL
 51 HYIPIRVLGR GAPGEATLYR RTEDDSLVLVW KEVDLTRLSE KERRDALNEI
 101 VILALLQHDN IIAYYNHFMD NTLLEIELEY CNGGNLYDKI LRQKDKLFEE
 151 EMVVWYLFQI VSAVSCIHKA GILHRDIKTL NIFLTKANLI KLG DYGLAKK
 201 LNSEYSMAET LVGTPYYMSP ELCQGVKYNF KSDIWA VGC V IFELLTLKRT
 251 FDATNPLNLC VKIVQGIRAM EVDSSQYSLE LIQMVHSCLD QDPEQRPTAD
 301 ELLDRPLLRK RRREMEEKVT LLNAPTKRPR SSTVTEAPIA VVTSRTSEVY
 351 VWGGGKSTPQ KLDVIKSGCS ARQVCAGNTH FAVVTVEKEL YTWVNMQGGT
 401 KLHGQLGHGD KASYRQPKHV EKLQ GKAIHV VSCGDDFTVC VTDEGQLYAF
 451 GSDYYGCMGV DKVAGPEVLE PMQLNFFLSN PVEQVSCGDN HVVVLTRNKE
 501 VYSWGCGEYG RLGLDSEEDY YTPQKVDVPK ALIIVAVQCG CDGTFLLTQS
 551 GKVLACGLNE FNKLGLNQCM SGIINHEAYH EVPYTTSTFTL AKQLSFYKIR
 601 TIAPGKTHTA AIDERGRLLT FGCNKCGQLG VGNYYKRLGI NLLGGPLGGK
 651 QVIRVSCGDE FTIAATDDNH IFAWGNGNG RLAMTPTERP HGSDICTSWP
 701 RPIFGLHHV PDLSCRGWHT ILIVEKVLNS KTIRSNSSSL SIGTVFQSSS
 751 PGGGGGGGGG EEEDSQESE TPDPSGGFRG TMEADRGMEG LISPTAMGN
 801 SNGASSSCPG WLRKELENAE FIPMPDSPSP LSAAFSESEK DTLPYEELQG
 851 LKVASEAPLE HKPQVEASSP RLNPVATCAG KGTPLTPPAC ACSSLQVEVE
 901 RLQGLVLKCL AEQQKLQZEN LQIFTQLQKL NKKLEGGQQV GMHSGKTQTA
 951 KEEMEMDPKP DLSDSWCLL GTDSCRPSL*

FIGURE 4

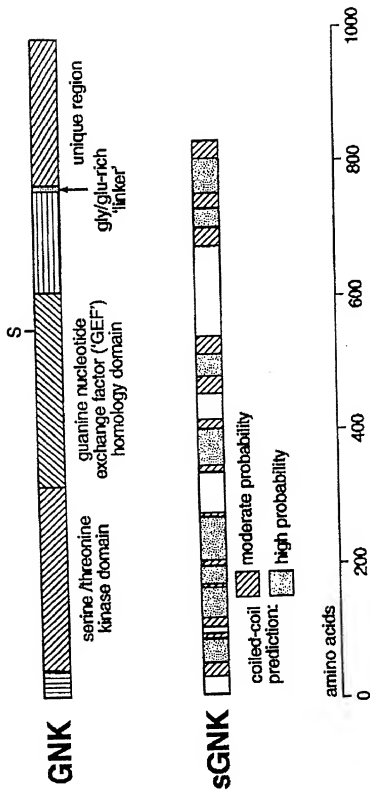


FIGURE 5

Putative GNK Domains and Structural Features

KINASE (44-315)

GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) (318-605)

GLYCINE/ACIDIC-RICH TETHER (752-764)

C-TERMINAL DOMAIN WITH NO KNOWN HOMOLOGY OR FUNCTION (765-979)

1 MSVLGEYERH CDSINSDFGS ESGGCGDSSP GPSASQGPRA GGGAAEQEEL
51 HYIPIRVLGR GAFGEATLYR RTEDDSLVLVW KEVDLTRLSE KERRDALNEI
101 VILALLQHDN IIAYYNHFMD NTLLIELEY CNGGNLYDKI LRQKDKLFEE
151 EMVWVYLFOI VSAVSCIHA GILHRDIKTL NIFLTKANLI KLG DYGLAKK
201 LNSEYSMAET LVGTPPYMSP ELCQGVKYNF KSDIWA VGC V IPELLTLKRT
251 FDATNPLNLC VKIVQIRAM EVDSSQSYSE LIQMVHSCLD QDPEQRPTAD
301 ELLDRPLLRK RRREMEEKVT LLNAPTKRPR SSTVTEAPIA VVTSRTSEVY
351 VWGGGKSTPO KLDVIKSGCS AROVCAGNTH FAVVTVEKEL YTWVNMGGGT
401 KLHGOLGHGD KASYROPKHV EKLOGKAIHQ VSCGDDFTVC VTDEGOLYAF
451 GSDYYGCMGV DKVAGPEVLE PMOLNFFLSN PVEQVSCGDN HVVVLTRNKE
501 VYSWGCGEYG RLGLDSEEDY YTPOKVDVPK ALIIVAVOCG CDGTFLLTQS
551 GKVLACGLNE FNKLGINOCM SGINHEAYH EVPYTTSFTL AKQLSFYKIR
601 TIAPGKTHTA AIDERGRLLT FGCNKGQLG VGNKKRLGI NLLGGPLGGK
651 QVIRVSCGDE FTIAATDDNH IFAWNGGNG RLAMTPTERP HGS DICTSWP
701 RPIFGSLHHV PDLSCRGWHT ILIVEKVLNS KTIRSNSSGL SIGTVFQSSS
751 PGGGGGGGGG EEEDSQOQSE TPDPSGGFRG TMEADRGMEG LISPTTEAMGN
801 SNGASSSCPG WLRKELENAE FIPMPDSPSP LSAAFSESEK DTLPYEELQG
851 LKVASEAPLE HKPOVEASSP RLNPVAVTCAG KGTPLTTPAC ACSSLOVEVE
901 RLQGLVLKCL AEOQKLOQEN LOIFTQLQKL NKKLEGGQOV GMHSGKTOTA
951 KEEMEMDPKP DLDSDSWCLL GTDSCRPSL

FIGURE 6

Bicaudal D -----MAAEEVLQTVHDY
 sGNK -----MSAPSEEEYVARIVMAQEFLW
 C-NAP1 (aa 121) NTHLEAQLQKABEAGAEIQADLRDIQEKEEIKKKLSESRHQQAATTQLQLHQEAKRQ

Bicaudal D KTEIERLTKELTETTHEKIQAAEYGLVLEEKLTLLKQYDELEAEYDSLKQLEQLKEAF
 sGNK RAEEVRLSHELAEITTEKIQAAEYGLAVLEEKHLKQLQFELEVDYEAIRSEMEQLKEAF
 C-NAP1 EEVLRAVQEKEALVREKAAELVRLQAEVDRDQLABQLQLQESAKLESSLFEAQQQN

Bicaudal D GQSFSIHRKVAEDCETREETLLQESASKEAYYLKGLILEMQLNELKQSRVAVTVQQAENRL
 sGNK GQAHNTNKKVAADGESREESLIQESASKEQYVVRKVLLELQTELKQLRNVLTNTQSENRL
 C-NAP1 SVIEVTGKQLEVQIQTVTAKEVIQGEVRCLELDELDTERSQAE-QERDAAARQLAQAEQE

Bicaudal D TAVVQDLKENNEVVELQRIKRNKDEIREYKFPREARLLQDYTELEENITPLQKLVSTLKQKQ
 sGNK ASVQELKEINQVETLQGRRLRDIKRYKFPREARLLQDYSELEENITSLQKQSVLRQKQ
 C-NAP1 GKTALEQQKAAAEKEVNLREKWE-KERSWHQQLAKALESLEREKMELEMLRKEQE-QTE

Bicaudal D VEYEGLKHEIKRFEETVLLNSQLEDAIRLKEIAEHOLEBALETIKNEREQKNLRKELS
 sGNK VEFEGLKHEIKRFEETVLLNSQLEDAIRLKEISERQLEBALETIKTEREQKNLRKELS
 C-NAP1 MEAIQAQREERTQAESALCQMQLTEKERVSLLETLLQTKELADASQQLERLRQDMKV

Bicaudal D QYISLND----NHISISVDGLKFAEDGSEFNN--DDKMNHGHIHGPLVKLNGDYRTPTLRK
 sGNK HYMSINDSPYTHSLHVSIDLGLKFPDDAAEFNNDAAELVNGPEHGGALQLELDNKSTSTPKK
 C-NAP1 QKLKEQETTGILQTLQLEAQRELKEAARQHRDLAALQESSSSLQDMQLQKQVEDLKS

Bicaudal D ---GSELNPFVSLDFSELNITSEIQKLQQLMQVEREKAILLANLQESQGLEHTKGALE
 sGNK EQLAPPPSPSLVSDLLSELNITSEIQKLQQLMQVEREKAILLANLQESQGLEHTKGALE
 C-NAP1 QLVAQDSDSRLVEQEVEQKLEKLETFQYNNRIQKLELEREKAASLTLSLEMEKELVLVLEQADSI

Bicaudal D QHEVRHLTEHVNAMRGLQSSKELKAELEDGKGRDSGEEAHDYEVINDGLEILECKYRVA
 sGNK QKEKVTRLTENLSALRRLQASKERQTALDNEKDRSDSHEDGYYEVDINDGLEILACKYHVA
 C-NAP1 RQQLSALRQDMQAQGEQKELSAQMEILLRQEVKE-EDAPLQEAQLELEEAASHITEQ

Bicaudal D VTEVIDLKABIKALKEKYNKSVENYTDKAKYESKIQMYDEQVTSLEKTTKESGEMAHM
 sGNK VAEAGEELREQLKALRSTHEAREAQHAEEKGRYEAEGQALTEKYSILLEKASQRDRELLARL
 C-NAP1 QLRLASLWAQEAQAAQLQLRLRSTESQLEALAAEQPGNQQAQQAQSLYSALQQAQGSV

Bicaudal D EKELQKNTSTANENHSTLNTAQDELVTFFSELAQLYHHVCLCNNEFPNRMVLDYYRQSRV
 sGNK EKELKYSVDAGEQTGSLVAQDELVTFFSELANLVHHVCMCNNEFPNRMVLDYYREG--
 C-NAP1 CESRPELSCGSDSAPSVWGLEPDPQNG--ARSLFKRGPILLTASAEVASALHKLHQLDLK

Bicaudal D TRSGSLKGPDDPROLLSPRLARRGVSSPVTETRSSEPVAKESTEPSKEPSPTKTPTISPV
 sGNK -QGG--AGRTSPGGRTSP--EARGRRSPILL----PKGLLAPEAGRADGGTGDSDSPSPG
 C-NAP1 TQQTREDVLRDQVQKLEERLTDTEAKESQVHTELQDLQRLQSLQHQEESKWBEGKQNSLESE

Bicaudal D ITAPSPSPVLDSDIRKEPMNIYNLNAIIRDQIKHLQKAVDRSLQSLRQRAAARELAPMT
 sGNK SSLP--SPLSDF--RR-EPMNIYNLAIIRDQIKHLQKAVDRSLQSLRQRAAARELAPMT
 C-NAP1 LDKHETMASLQSLRRAELQREMAQGER---ELLQAAKNETLAQVEHLQAAVVEARAQ

Bicaudal D DKDKKALMEELIKLKLSTLKREQIATLRAVLKANKQTAFAVALANLKSKYENKAMVET
 sGNK DKDKKALMEELIKLKLSTLKREQIATLRAVLKANKQTAFAVALANLKSKYENKAMVET
 C-NAP1 ASAAQILEEDLRTARSALKLNKEEVESERERAQALQEQLQELQVAKALQEN-LALLTQT

Bicaudal D MTKLRNELKALKEDAAFTSSLRMTFATRCDEYVTLQDENQRQLAAAEDEKKTINTLLRMA
 sGNK MTKLRNELKALKEDAAFTSSLRMTFATRCDEYVTLQDENQRQLAAAEDEKKTINTLLRMA
 C-NAP1 LAEREVEETVLAGIQIELEKQREMQAALLESLSLDKKRNGVEDVLQEQEQTQLEKCRSLV

Bicaudal D IQQKALATQRLELEDFHDEQSRSSGKGLG-KSKIGSPKV (-> 154 aa)
 sGNK IQQKALATQRLELEDFHDEQTRGRAKAAPKPAFESL*-----
 C-NAP1 EHLPMAVQEREGKLTVQREQIRELEKDRGTQNVLEHQL (-> 914 aa)

Comparison of sGNK with coiled-coil domains of Human Bicaudal D and the human centrosomal NEK-1 substrate protein C-Nap1

FIGURE 7

sGNK is a substrate for GNK *in vitro*.

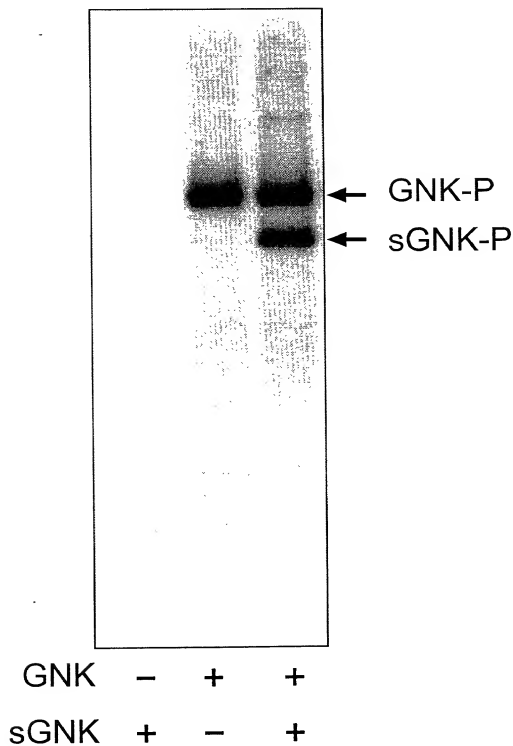


FIGURE 8

Final GNK purification step:
microbore Mono Q column chromatography

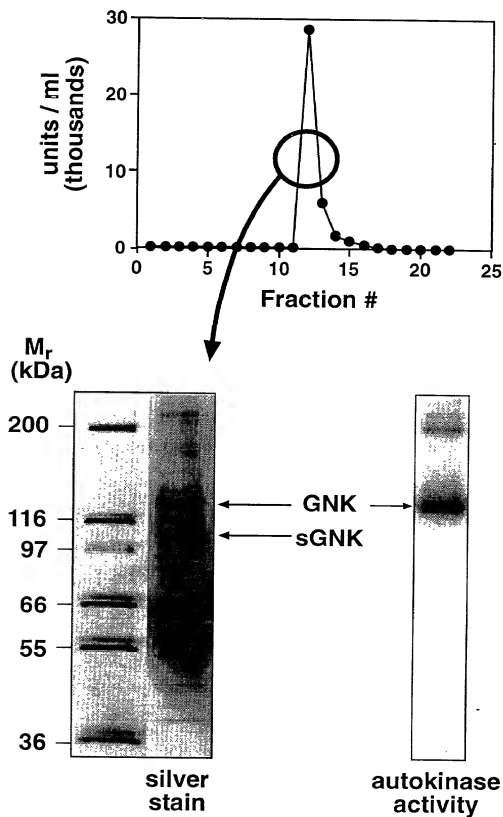


FIGURE 9

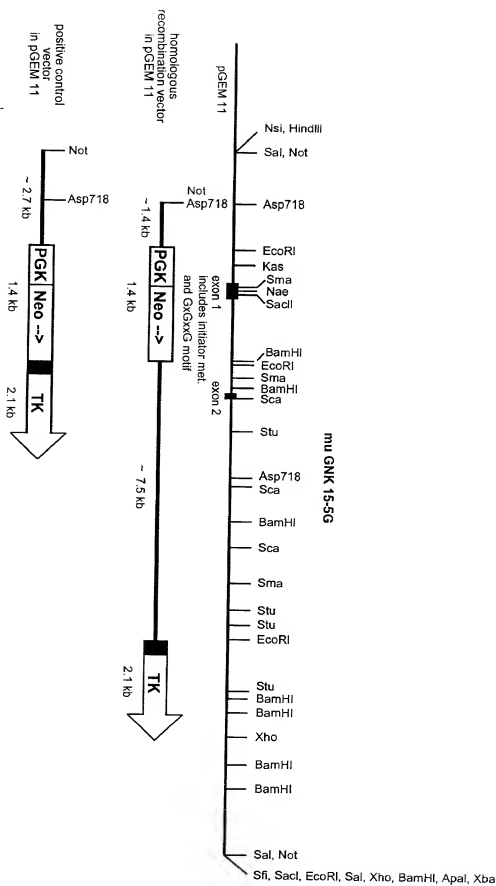


FIGURE 10

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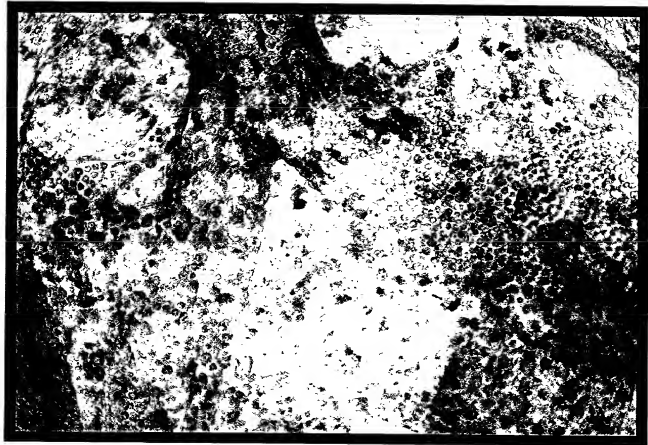


FIGURE 11A (top)
FIGURE 11B (bottom)